

SEQUENCE LISTING

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tti Phe 95	ggg Gly	gtg Val	aag Lys	ttg Leu	tac Tyr 100	cct Pro	gct Ala	ggt Gly	gcc Ala	acg Thr 105	aca Thr	aat Asn	tct Ser	caa Gln	gat Asp 110	338
gga Gl	ı gtg Val	act Thr	gat Asp	ctt Leu 115	ttc Phe	Gly	aag Lys	tgt Cys	tta Leu 120	cca Pro	gtt Val	cta Leu	caa Gln	gaa Glu 125	atg Met	386
	gag Glu															434
gaq	gtt Val	gac Asp 145	atg Met	ttt Phe	gat Asp	aga Arg	gaa Glu 150	aag Lys	gta Val	ttc Phe	att Ile	gaa Glu 155	acg Thr	gtt Val	cta Leu	482
	ccg Pro 160															530
gt: Va: 175	acc Thr	acc Thr	att Ile	gat Asp	gct Ala 180	gtt Val	aag Lys	ttt Phe	gtt Val	gaa Glu 185	tct Ser	tgc Cys	act Thr	gaa Glu	gga Gly 190	578
	gtt Val															626
tct Sei	ctc Leu	ttc Phe	caa Gln 210	ggg Gly	ggc Gly	tta Leu	caa Gln	ccg Pro 215	cat His	aat Asn	tac Tyr	tgc Cys	ctt Leu 220	cca Pro	gtc Val	674
cto Lev	aaa Lys	aga Arg 225	gag Glu	atc Ile	cac His	agg Arg	gag Glu 230	gca Ala	ctť Leu	gtg Val	tca Ser	gct Ala 235	gta Val	aca Thr	agt Ser	722
	agt Ser 240															770
	aga Arg															818
gta Val	gcc Ala	ttg Leu	tca Ser	gta Val 275	tat Tyr	gcg Ala	aag Lys	gtg Val	ttt Phe 280	gaa Glu	aag Lys	gaa Glu	aat Asn	gca Ala 285	ctc Leu	866
	aag Lys															914
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Thr Ile Asp Ala Val Lys Phe Val Glu Ser Cys Thr Glu Gly Phe Val

Ala Ala Thr Val Thr Pro Gln His Leu Val Leu Asn Arg Asn Ser Leu . 195 Phe Gln Gly Gly Leu Gln Pro His Asn Tyr Cys Leu Pro Val Leu Lys Arg Glu Ile His Arg Glu Ala Leu Val Ser Ala Val Thr Ser Gly Ser 225 Lys Arg Phe Phe Leu Gly Thr Asp Ser Ala Pro His Asp Arg Arg Arg Lys Glu Cys Ser Cys Gly Cys Ala Gly Ile Tyr Asn Ala Pro Val Ala Leu Ser Val Tyr Ala Lys Val Phe Glu Lys Glu Asn Ala Leu Asp Lys Leu Glu Ala Phe Thr Ser Phe Asn Gly Pro Asp Phe Tyr Gly Leu Pro Arg Asn Asn Ser Lys Ile Lys Leu Ser Lys Thr Pro Trp Lys Val Pro Glu Ser Phe Ser Tyr Ala Ser Gly Asp Ile Ile Pro Met Phe Ala Gly 330 Glu Met Leu Asp Trp Leu Pro Ala Pro Leu <210> 3 <211> 1962 <212> DNA <213> Nicotiana tabacum <220> <221> CDS <222> (305)..(1678) <400> 3 gaatteggea egageacaaa agtagaaagg gttttgetet eeeettteat etgtgtetea 60 taactgtgct aaaacctctc ccatcttccc tcaagaacaa agccacccca aaacaccacc 120 ttgtacactc ccattgtcgc ttccagtttt gtgccccaaa taaccttttc agtcatttgt 180 atcttagcat caacaacagt tgctgtctct cttttgttcg tccaatatac tgagcatttt 240 ttgagtagta atttgaaggg tttattcagt tgttaaatat ttgatttttg ttttgtttaa 300 gaaa atg aga caa agg gtt gga ttt gca ttg att aga gaa agc ttg tat Met Arg Gln Arg Val Gly Phe Ala Leu Ile Arg Glu Ser Leu Tyr cgt aag cta aaa cca agc tct gtt ccc aga cat tat tgc act tct tct Arg Lys Leu Lys Pro Ser Ser Val Pro Arg His Tyr Cys Thr Ser Ser

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ggg Gly	gga Gly 65	gct Ala	tat Tyr	gca Ala	agt Ser	acg Thr 70	gtt Val	gat Asp	gag Glu	gcc Ala	acc Thr 75	ttc Phe	tgt Cys	ggc Gly	tgg Trp	541
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cca Pro	gag Glu	gtt Val	gct Ala	cac His 100	aaa Lys	ctg Leu	gcg Ala	gtc Val	tct Ser 105	gct Ala	gca Ala	gcc Ala	cga Arg	gga Gly 110	tgg Trp	637
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cag Gln	cat His	ggt Gly 210	aag Lys	aga Arg	aag Lys	ttg Leu	gaa Glu 215	aca Thr	tct Ser	agt Ser	act Thr	tca Ser 220	tct Ser	cca Pro	gct Ala	973
gga Gly	gat Asp 225	gaa Glu	gtc Val	aag Lys	cat His	gga Gly 230	ggg Gly	aaa Lys	gct Ala	ggt Gly	cct Pro 235	ggt Gly	att Ile	ctt Leu	ggt Gly	1021
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cca gat tcc Pro Asp Ser				l Ala							1405
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tca atc agt Ser Ile Ser 450						tagt	agta	igt t	gata	ıtacta	1698
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Lys Gly Arg Leu Phe Thr Gly Ala Thr Ile Gly Leu Leu Ile Ala Gly 50 60

Gly Ala Tyr Ala Ser Thr Val Asp Glu Ala Thr Phe Cys Gly Trp Leu 65 70 75 80

Phe Ser Ala Thr Lys Leu Val Asn Pro Phe Phe Ala Phe Leu Asp Pro 85 90 95

Glu Val Ala His Lys Leu Ala Val Ser Ala Ala Ala Arg Gly Trp Val 100 105 110

Pro Arg Glu Lys Arg Pro Asp Pro Pro Ile Leu Gly Leu Asp Val Trp 115 120 125

Gly Arg Arg Phe Ser Asn Pro Val Gly Leu Ala Ala Gly Phe Asp Lys 130 135 140

Asn Ala Glu Ala Val Glu Gly Leu Leu Gly Leu Gly Phe Gly Phe Val 145 150 155 160

Glu Val Gly Ser Val Thr Pro Ile Pro Gln Glu Gly Asn Pro Lys Pro 165 170 175

Arg Ile Phe Arg Leu Pro Asn Glu Gly Ala Ile Ile Asn Arg Cys Gly 180 185 190

Phe Asn Ser Glu Gly Ile Val Val Val Ala Lys Arg Leu Gly Ala Gln 195 200 205

His Gly Lys Arg Lys Leu Glu Thr Ser Ser Thr Ser Ser Pro Ala Gly 210 215 220

Asp Glu Val Lys His Gly Gly Lys Ala Gly Pro Gly Ile Leu Gly Val 225 230 235 240

Asn Leu Gly Lys Asn Lys Thr Ser Glu Asp Ala Ala Asp Tyr Val 245 250 255

Gln Gly Val His Thr Leu Ser Gln Tyr Ala Asp Tyr Leu Val Ile Asn Ile Ser Ser Pro Asn Thr Pro Gly Leu Arg Gln Leu Gln Gly Arg Lys Gln Leu Lys Asp Leu Val Lys Lys Val Gln Ala Ala Arg Asp Glu Met Gln Trp Gly Glu Gly Pro Pro Pro Leu Leu Val Lys Ile Ala Pro Asp Leu Ser Lys Gln Asp Leu Glu Asp Ile Ala Val Val Ala Val Ala 330 Leu Arg Val Asp Gly Leu Ile Ile Ser Asn Thr Thr Val Gln Arg Pro Asp Ser Ile Ser Gln Asn Pro Val Ala Gln Glu Ala Gly Gly Leu Ser Gly Lys Pro Leu Phe Asp Met Ser Thr Asn Ile Leu Lys Glu Met Tyr Val Leu Thr Lys Gly Arg Ile Pro Leu Ile Gly Thr Gly Gly Ile Ser 395 Ser Gly Glu Asp Ala Tyr Lys Lys Ile Arg Ala Gly Ala Thr Leu Val 410 Gln Leu Tyr Thr Ala Phe Ala Tyr Gly Gly Pro Ala Leu Ile Pro Asp 425 Ile Lys Asp Glu Leu Ala Arg Cys Leu Glu Lys Asp Gly Tyr Lys Ser Ile Ser Glu Ala Val Gly Ala Asp Cys Arg <210> 5 <211> 15 <212> PRT <213> Artificial Sequence <223> by peptide synthesis <400> 5 Leu Gly Thr Asp Ser Ala Pro His Asp Arg Arg Arg Lys Glu Cys <210> 6 <211> 26

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